

FIG. 1A

(SEQ ID NO: 1) →

5' CAG ACT CAC GGT CAA GCT AAG GCG AAG AGT GGG TGG CTG AAG CCA TAC TAT TTT

ATA GAA TTA ATG GAA AGC AGA AAA GAC ATC ACA AAC CAA GAA GAA CTT TGG AAA

(SEQ ID NO: 2) → M E S R K D I T N Q E E L W K

ATG AAG CCT AGG AGA AAT TTA GAA GAA GAC GAT TAT TTG CAT AAG GAC ACG GGA

M K P R R N L E E D D Y L H K D T G

GAG ACC AGC ATG CTA AAA AGA CCT GTG CTT TTG CAT TTG CAC CAA ACA GCC CAT

E T S M L K R P V L L H L H Q T A H

GCT GAT GAA TTT GAC TGC CCT TCA GAA CTT CAG CAC ACA CAG GAA CTC TTT CCA

A D E F D C P S E L Q H T Q E L F P

CAG TGG CAC TTG CCA ATT AAA ATA GCT GCT ATT ATA GCA TCT CTG ACT TTT CTT

Q W H L P I K I A A I I A S L T F L

TAC ACT CTT CTG AGG GAA GTA ATT CAC CCT TTA GCA ACT TCC CAT CAA CAA TAT

X T L L R E V I H P L A T S H Q Q Y

TTT TAT AAA ATT CCA ATC CTG GTC ATC AAC AAA GTC TTG CCA ATG GTT TCC ATC

F Y K I P I L V I N K V L P M V S I

ACT CTC TTG GCA TTG GTT TAC CTG CCA GGT GTG ATA GCA GCA ATT GTC CAA CTT

T L L A L V Y L P G V I A A I V Q L

CAT AAT GGA ACC AAG TAT AAG AAG TTT CCA CAT TGG TTG GAT AAG TGG ATG TTA

H N G T K Y K K F P H W L D K W M L

ACA AGA AAG CAG TTT GGG CTT CTC AGT TTC TTT TTT GCT GTA CTG CAT GCA ATT

T R K O F G L L S F F F A (V) L H A I

TAT AGT CTG TCT TAC CCA ATG AGG CGA TCC TAC AGA TAC AAG TTG CTA AAC TGG

Y S L S Y P M R R S Y R Y K L L N W

184 192

⁶⁵⁹ GCA TAT CAA CAG GTC ⁶⁸⁸ CAA CAA AAT ⁶⁷⁷ AAA GAA GAT ⁶⁸⁶ GCC TGG ATT ⁸⁹⁵ GAG CAT ⁷⁰⁴ GAT GTT
 A Y Q Q V Q Q N K E D A W I E H D V
⁷¹³ TGG AGA ⁷¹² ATG GAG ATT ⁷³¹ TAT GTG TCT ⁷⁴⁰ CTG GGA ATT ⁷⁴⁹ GTC GGA TTG ⁷⁵⁸ GCA ATA CTG GCT
 W R M E I Y V S L G I V G L A I L A
⁷⁶⁷ CTG TTG GCT ⁷⁷⁶ GTG ACA TCT ATT ⁷⁸⁵ CCA TCT ⁷⁹⁴ GTG AGT GAC TCT ⁸⁰³ TTG ACA ⁸¹² TGG AGA GAA
 L L A V T S I P S V S D S L T W R E
⁸²¹ TTT CAC TAT ATT ⁸³⁰ CAG AGC AAG CTA ⁸³⁹ GGA ATT GTT ⁸⁴⁸ TCC CTT CTA ⁸⁵⁷ CTG GGC ⁸⁶⁶ ACA ATA
 F H Y I O S K L G I V S L L L G T I
⁸⁷⁵ CAC GCA TTG ATT TTT ⁸⁸⁴ GCC TGG AAT ⁸⁹³ AAG TGG ATA ⁹⁰² GAT ATA ⁹¹¹ AAA CAA ⁹²⁰ TTT GTA TGG
 H A L I F A W N K W I D I K Q F V W
⁹²⁹ TAT ACA CCT CCA ACT ⁹³⁸ TTT ATG ATA ⁹⁴⁷ GCT GTT TTC ⁹⁵⁶ CTT CCA ATT ⁹⁶⁵ GTT GTC ⁹⁷⁴ CTG ATA
 Y T P P T F M I A V F L P I V V L I
⁹⁸³ TTT AAA AGC ATA CTA ⁹⁹² TTC CTG CCA TGC ¹⁰⁰¹ TTG AGG AAG ¹⁰¹⁰ AAG ATA ¹⁰¹⁹ CTG AAG ¹⁰²⁸ ATT AGA
 E K S I L F L P C L R K K I L K I R
¹⁰³⁷ CAT GGT TGG ¹⁰⁴⁶ GAA GAC GTC ¹⁰⁵⁵ ACC AAA ATT ¹⁰⁶⁴ AAC AAA ACT ¹⁰⁷³ GAG ATA TGT ¹⁰⁸² TCC CAG TTG
 H G W E D V T K I N K T E I C S Q L
¹⁰⁹¹ TAG AAT TAC TGT ¹¹⁰⁰ TTA CAC ACA TTT ¹¹⁰⁹ TTG TTC AAT ATT ¹¹¹⁸ GAT ATA ¹¹²⁷ TTT TAT ¹¹³⁶ CAC CAA
 * N Y C L H T F L F N I D I F Y H Q
¹¹⁴⁵ CAT TTC AAG TTT ¹¹⁵⁴ GTA TTT ¹¹⁶³ GTT AAT ¹¹⁷² AAA ATG ATT ¹¹⁸¹ ATT CAA ¹¹⁹⁰ GGA AAA AAA AAA AAA
 H F K F V F V N K M I I Q G K K K K

AAA AA 3'

K

FIG. 1B

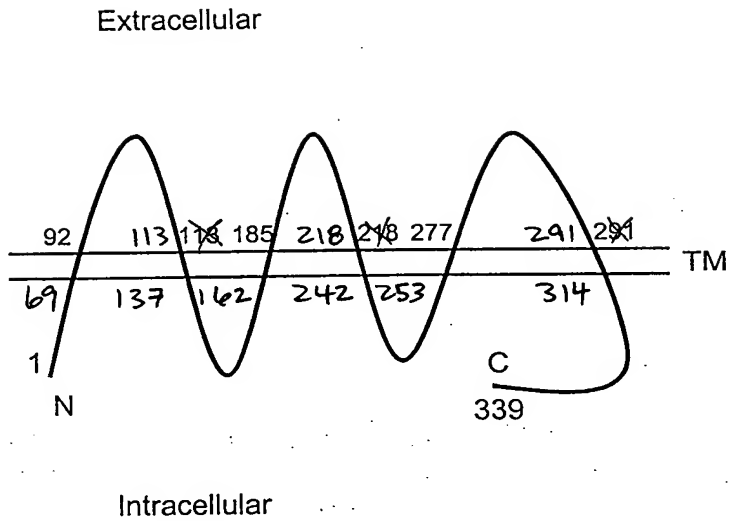


FIG. 1C

5' GGC GGA GGC GGA GGC GGA GGG CGA GGG GCG GGG AGC GCC GCC TGG AGC GCG
GCA GGT CAT ATT GAA CAT TCC AGA TAC CTA TCA TTA CTC GAT GCT GTT GAT
AAC AGC AAG 3' (SEQ ID NO: 3)

FIG. 4 - 1

GGGGCCCGCACCTCTGGGCAGCAGCGGCAGCCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCC
ATACTATTTTATAGAATTAATGGAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGG
AGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGC
ATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACCTCTTCCACA
GTGGCACTTGCCAATTAATAAGCTGCTATTATAGCATCTCTGACTTTTCTTTTACACTCTTCTGAGGGAAGTAATT
CACCCCTTAGCAACTTCCCATCAACAATATTTTATAAAATTCGAATCCTGGTCATCAACAAAGCTTTGCCAATGG
TTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACCTTCATAATGGAACCAA
GTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTT
GCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCAT
ATCAACAGGTCCAACAAAATAAAGAAGATGCCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCT
GGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGG
AGAGAATTTCACTATATTCAGGTAATAATATATAAAATAACCCCTAAGAGGTAATCTTCTTTTTGTGTTTATGAT
ATAGAATATGTTGACTTTACCCCAATAAAAAATAACAAATGTTTTTCAACAGCAAAGATCTTATACTTGTTCGAATT
AATAATGTGCTCTCCTGTTGTTTTCCCTATTGCTTCTAATTAGGACAAGTGTTTCTAGACATAAATAAAGGCAT
TAAAAATATCTTTGTTTTTTTTTTTTGTTTGTGTTGTTTTGTTTGTGTTGTTTTTGGAGATGAAGTCTCG
CTCTGTTGCCCATGCTGGAGTACAGTGGCAGATCTCGGCTCACTGCAACCTGCGCCTCCTGGGTTTCAGGCGATTC
TCTTGCCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACCCATCACCATGTCCAGCTAATTTTGTATTTTAGTA
GAGACAGGGTTTTCCCATGTTGGCCAGGCTGGTCTCGATCTCCTGACCTCAAATGATCCGCCCACCTCGGCCTCCC
AAAGTGCTGGGATGACAGTTGTGAGCCACCACACTCAGCCTGCTCTTTCTAATATTTGAAACTTGTTAGACAATTT
GCTACCCATCTAATGTGATATTTTAGGAATCCAATATGCATGGTTATTATTCTTAAAAAAATATTCTTTTACC
TGTCACCTGAATTTAGTAATGCCTTTTATGTTACACAACTTAGCACTTTCCAGAAACAAAACCTCTCTCCTTGAAA
TAATAGAGTTTTTATCTACCAAAGATATGCTAGTGTCTCATTTCAAAGGCTGCTTTTCCAGCTTACATTTTATAT
ACTTACTCACTGAAGTTTCTAAATATTCTTGTAATTTTAAACATCTCAGATTACTGAGGTTTATCTTCTGGT
GGTAGATTATCCATAAGAAGAGTGATGTGCCAGAATCACTCTGGGATCCTGTCTGACAAGATTCAAAGGACTAAA
TTTAATTCAGTCATGAACACTGCCAATTACCGTTTATGGGTAGACATCTTGGAAATTTCCACAAGGTGAGACATT
CGCAACTATCCCTTCTACATGTCCACAGTATACTCCAACACTTTATTAGGCATCTGATTAGTTTGAAAGTATGC
CTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGGTACAACATTCTCAGAAATTTCTAATTTGTAGGTTTCAG
CCTGATAACCACTGGAGTTCTTTGGTCCTCATTAAATAGCTTTCTTCACACATTGCTCTGCCTGTTACACATATGA
TGAACACTGCTTTTTAGACTTCCATTAGGAATTTAGGACTGCATCTTGACAACTGAGCCTATTCTACTATATGTACA

FIG. 4-2

ATACCTAGCCCATAAATAGGTATACAATACACATTTGGTAAACTAATTTTCAACCAATGACATGTATTTTCAACT
AGTAACCTAGAAATGTTTCACTTAAATCTGAGAACTGGTTACACTACAAGTTACCTTGGAGATTCAATATATGAAA
ACGCAAACTTAGCTATTTGATTGTATTCAGTGGGACTTAAGAATGCGCCTGAATAATTGTGAGTTCGATTTGTTCT
GGCAGGCTAATGACCATTTCAGTAAAGTGAATAGAGGTCAGAAGTCGTATAAAAGAGGTGTTGTCAGAACCCGT
TGAGATTACATAGGTGAACAATATTTTAAAGCAACTTTATTGTGTAGTGACAAAGCATCCCAATGCAGGCTGAA
ATGTTTCATCACATCTCTGGATCTCTCTATTTTGTGCAGACATTGAAAAAATTGTTTCATATTATTTCCATGTTATC
AGAATATTTGATTTTTTAAAAACATAGGCCAAGTTCATTCACTTCATTATTCATTATCAAAATCAGAGTGAATCA
CATTAGTCGCCTTCACAACTGATAAAGATCACTGAAGTCAAATTGATTTTTGTCTATAATCTTCAATCTACCTATAT
TTAATTGAGAATCTAAATGTACAAATCATTTGTGTTGATTCTGCAGTGATCCTGCTATAAGTAAGACTCAGTCCCT
GATTTTAGGTATCCTGTGAAAAGCAGAATTAAGACAAATACACAAGAGACAAAGCACAAAAATAAATATCATAAG
GGGATGAACAAAATGGTGGAGAAAGAGTAGACAAAGTTTTTGATCACCTGCCTTCAAAGAAAGGCTGTGAATTTG
TTCACCTTAGACAGCTTGGAGACAAGAAATTACCCAAAAGTAAGGTGAGGAGGATAGGCAAAAAGAGCAGAAAAGATG
TGAATGGACATTGTTGAGAAATGTGATAGGAAAACAATCATAGATAAAGGATTTCCAAGCAACAGAGCATATCCAG
ATGAGGTAGGATGGGATAAACTCTTATTGAACCAATCTTCACCAATTTTGTTTTCTTTTGCAGAGCAAGCTAGGA
ATTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATAAAACAATTTG
TATGGTATACACCTCCAACCTTTTATGATAGCTGTTTTCTTCCAATTGTTGTCTGATATTTAAAGCATACTATT
CCTGCCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTACCAAAATTAACAAAACCTGAG
ATATGTTCCCAAGTGTAGAAATTACTGTTTACACACATTTTGTTCATATTTGATATATTTTATCACCAACATTTCA
AGTTTGTATTTGTTAATAAAATGATTATTCAGGAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO:6)

FIG. 5

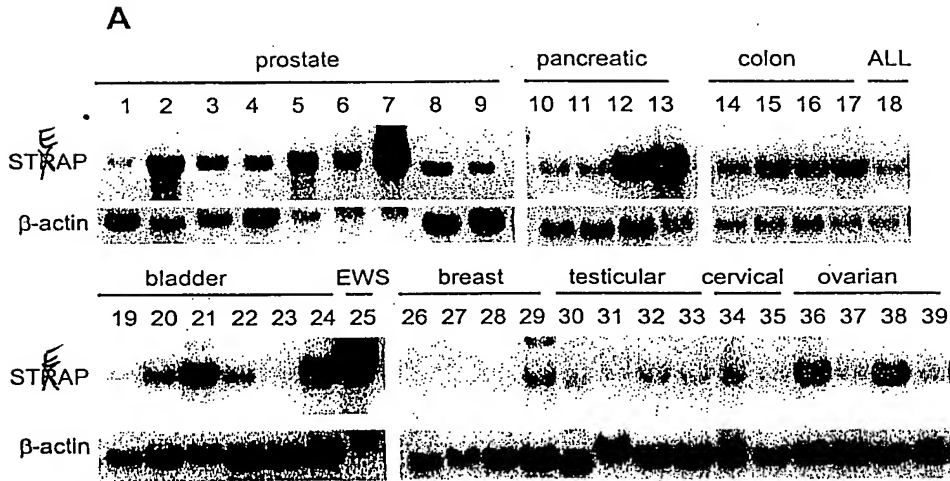
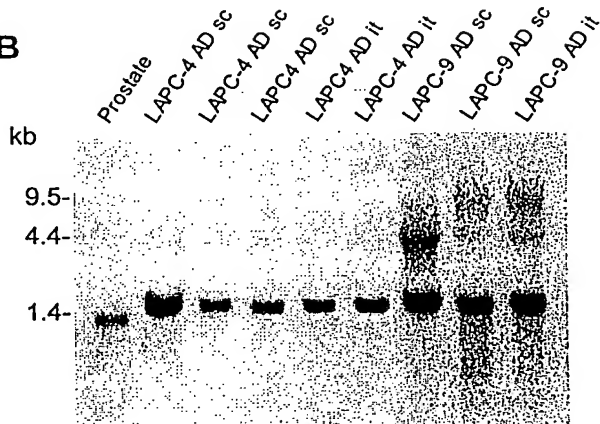
**B**

FIG. 6

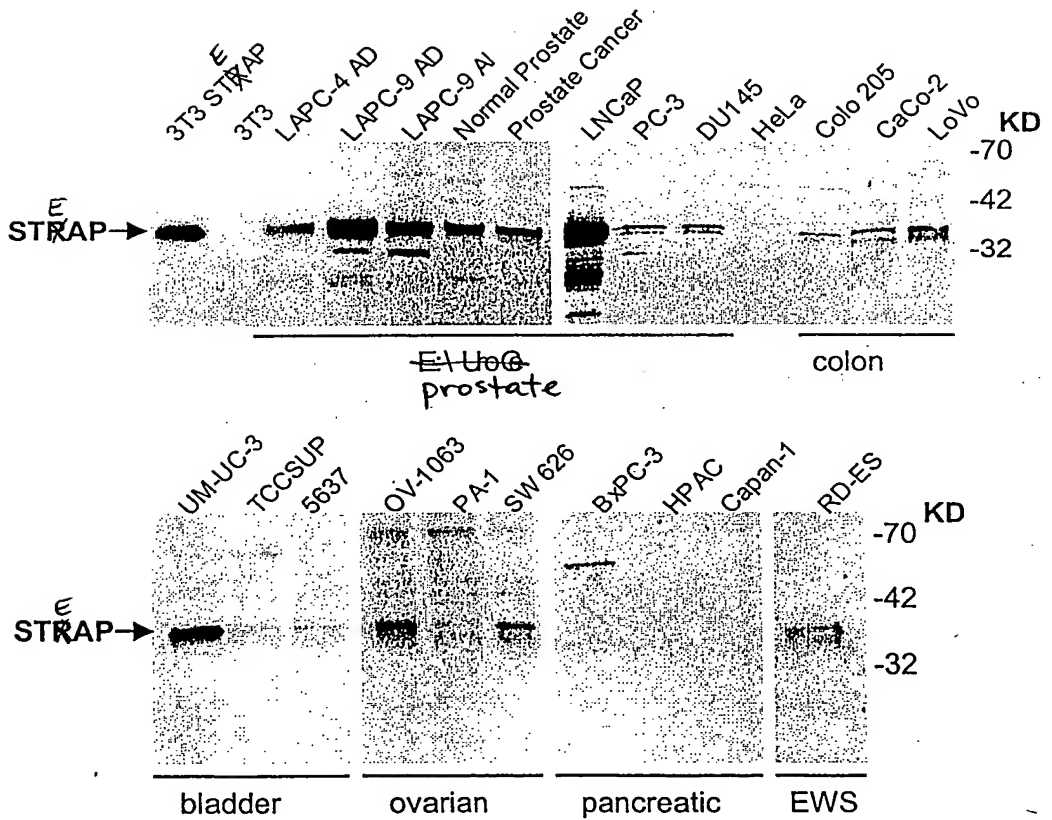
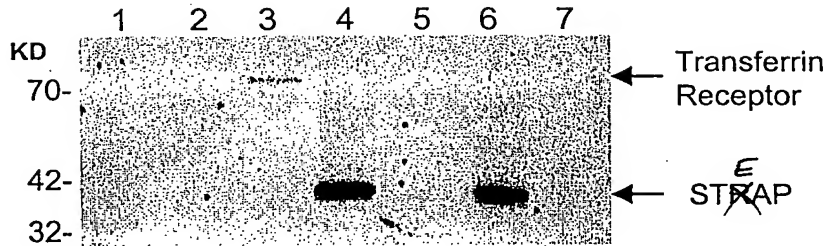


FIG. 7

A



B

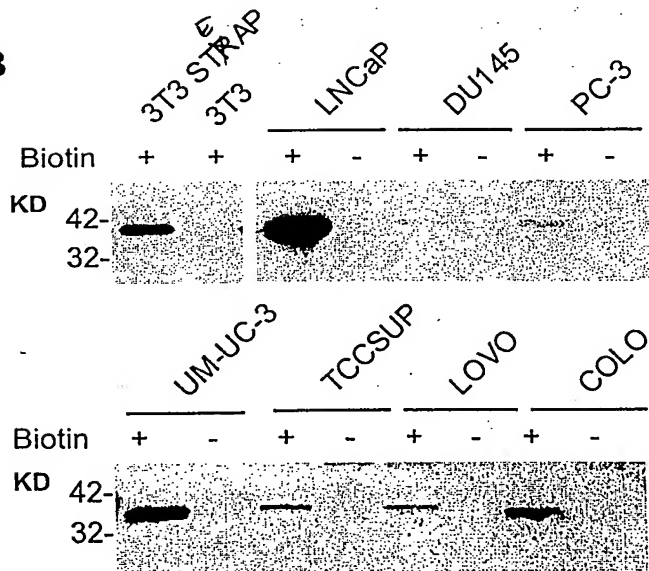


FIG. 9

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5'  GAC TTT 10      19      28      37      46      55
    --- --- TAC AAA ATT CCT ATA GAG ATT GTG AAT AAA ACC TTA CCT ATA GTT GCC
    Asp Phe Tyr Lys Ile Pro Ile Glu Ile Val Asn Lys Thr Leu Pro Ile Val Ala

      64      73      82      91      100      109
    ATT ACT TTG CTC TCC CTA GTA TAC CTC GCA GGT CTT CTG GCA GCT GCT TAT CAA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ile Thr Leu Leu Ser Leu Val Tyr Leu Ala Gly Leu Leu Ala Ala Ala Tyr Gln

      118      127      136      145      154      163
    CTT TAT TAC GGC ACC AAG TAT AGG AGA TTT CCA CCT TGG TTG GAA ACC TGG TTA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Leu Tyr Tyr Gly Thr Lys Tyr Arg Arg Phe Pro Pro Trp Leu Glu Thr Trp Leu

      172      181      190      199      208      217
    CAG TGT AGA AAA CAG CTT GGA TTA CTA AGT TTT TTC TTC GCT ATG GTC CAT GTT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Gln Cys Arg Lys Gln Leu Gly Leu Leu Ser Phe Phe Phe Ala Met Val His Val

      226      235      244      253      262      271
    GCC TAC AGC CTC TGC TTA CCG ATG AGA AGG TCA GAG AGA TAT TTG TTT CTC AAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ala Tyr Ser Leu Cys Leu Pro Met Arg Arg Ser Glu Arg Tyr Leu Phe Leu Asn

      280      289      298      307      316      325
    ATG GCT TAT CAG CAG GTT CAT GCA AAT ATT GAA AAC TCT TGG AAT GAG GAA GAA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Met Ala Tyr Gln Gln Val His Ala Asn Ile Glu Asn Ser Trp Asn Glu Glu Glu

      334      343      352      361      370      379
    GTT TGG AGA ATT GAA ATG TAT ATC TCC TTT GGC ATA ATG AGC CTT GGC TTA CTT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Val Trp Arg Ile Glu Met Tyr Ile Ser Phe Gly Ile Met Ser Leu Gly Leu Leu

      388      397      406      415      424      433
    TCC CTC CTG GCA GTC ACT TCT ATC CCT TCA GTG AGC AAT GCT TTA AAC TGG AGA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ser Leu Leu Ala Val Thr Ser Ile Pro Ser Val Ser Asn Ala Leu Asn Trp Arg

      442      451      460      469      478      487
    GAA TTC AGT TTT ATT CAG TCT ACA CTT GGA TAT GTC GCT CTG CTC ATA AGT ACT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Glu Phe Ser Phe Ile Gln Ser Thr Leu Gly Tyr Val Ala Leu Leu Ile Ser Thr

      496      505      514
    TTC CAT GTT TTA ATT TAT GGA TGG AAA CGA GCT 3' (SEQ ID NO: 7)
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Phe His Val Leu Ile Tyr Gly Trp Lys Arg Ala (SEQ ID NO: 8)

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FIG. 10

ε
 STRAP-2, AA508880 (NCI_CGAP Pr6)
 ggctcgacttttccctttattccctttgtcagagatctgattcatccatatgctagaaaccaacagagtgcacttttaca
 aaattccctatagagattgtgaataaaaccttacctatagttgccattactttgctctccctagatataccttgcagg
 tcttctggcagctgcttatcaactttattacggcaccagtaggagatttccaccttggttggaacacctgggta
 cagtgtagaaaacagcttggtacttaagttgtttcttcgctatggtccatggtgcctacagcctctgcttaccga
 tgagaaggctcagagagat (SEQ ID NO: 9)

ε
 STRAP-2, 98P4B6 SSH fragment
 TTTGCAGCTTTGCAGATACCCAGACTGAGCTGGAACTGGAATTGTCTTCTATTGACTCTACTTCTTTAAAGCG
 GCTGCCCATTTACATTCCTCAGCTGTCTTGCAGTTAGGTGTACATGTGACTGAGTGTGGCCAGTGAGATGAAGTC
 TCCTCAAAGGAAGGCAGCATGTGTCTTTTT (SEQ ID NO: 10)

AI139607 (testis EST)
 aagaaggagaatccatttagcacctcctcagcctggctcagtgattcatatgtggctttgggaataacttgggtttt
 ttctgtttgtactcttgggaatcacttctttgccatctgttagcaatgcagtcactggagagagttccgatttgt
 ccagtcctcaaacctgggttatattgacctgatcttgtgtacagccacacccctgggtgtacgggtgggaagagattccctc
 agcccttcaaatctcagatgggtatcttctgcagcctacgtgttagggcttatcattccttgcactgtgctgggtga
 tcaagtttgtcctaatacatgccatgtgtagacaacacctttacaaggatccgccagggtgggaaaggaaactcaaa
 acactagaaaaagcattgaatggaaaatcaatattttaaacaagttcaatttagctggaaaaaaaaa (SEQ ID NO: 11)

R80991 (placental EST)
 ggccgcggcancgctacgacctgggtcaacctggcagtcgaagcaggtcttggccanacaagagccacctctgggtg
 aaggaggaggtctggcggatggagatctacctctccctgggagtgtctggccctcggaacgttgtccctgctggcgg
 tgacctcactgcctccattgcaaaactcgtctcaactggaggaggttcagcttcgttcagtcctcactgggcttgt
 ggccntcgtgctgagcacactncacacgctcacctacggctggaccgcgccttcgaggagagccgctacaagttc
 tacctnctccaccttcaagntcacgctgctgggtgccctgctgttcctcctctgggccaagccctgttntac
 tgccttgcatccagccgnaga (SEQ ID NO: 12)

FIG. 11A

E
 STRAP-1 106 FYKIPILVINKVLPMSITLLALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWLTRKQFG
 STRAP-2 2 FYKIPIEIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPWLETWLQCRKQLG
 ***** * * * * *
 E
 STRAP-1 166 LLSFFFAVLHAIYSLSYPMRRSYRYKLLNWAYQQVQONKEDAWIEHDVWRMEIYVSLGIV
 STRAP-2 62 LLSFFFAMVHVAYSCLCPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIM
 ***** * * * * *
 E
 STRAP-1 226 GLAILALLAVTSIPSVSDSLTWREFHYIQSKLGIVSLLGTIHALIFAWN*
 STRAP-2 122 SLGLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKR
 * * * * *
 E
 (Portion of SEQ ID: 2)
 (Portion of SEQ ID: 8)

FIG. 11B

1	15 16	30 31	45 46	60 61	75 76	90
STRAP-1	MESKDIYNQELWK MKPRNLEEDDYLHK DTGETSMKRPVLJH LHQTAHADEFDCPSE LQHTQELFPQWHLPI KIAAIIASLTFLYTL					90
STRAP-2	-----					0
STRAP-3	-----					0
STRAP-4	-----					0
91	105 106	120 121	135 136	150 151	165 166	180
STRAP-1	LREVIHPLATSHOOY FYKIPILVINKVLPDM VSTIICALVILPCVIL KALVQDCHNGTKYKKK PHWILIKWMLTRKQFC DLSFFFANVLAHAKSL					180
STRAP-2	-----					76
STRAP-3	-----					0
STRAP-4	-----					0
181	195 196	210 211	225 226	240 241	255 256	270
STRAP-1	SVPHRRSRYKILNNA FYQOQOONKEDAWIE HDVWRMEIXVSLGIV GLAILANTCAVTSIPS VSDSLATWRETHYIOS MGLIVSLDOSTIHAL					270
STRAP-2	CLPHRUSRYKILNNA FYQOQOONKEDAWIE HDVWRMEIXVSLGIV GLAILANTCAVTSIPS VSDSLATWRETHYIOS MGLIVSLDOSTIHAL					166
STRAP-3	-----					68
STRAP-4	-----					82
271	285 286	300 301	315 316	330 331	345 346	360
STRAP-1	IFANWKWIDIKQFW YTPPIEMIAVPLPIV WLIPKSIILFPCIRK KILKIRHGWEDVTKI NKTEICSQL					339 (SEQ ID NO: 2)
STRAP-2	-----					173 (SEQ ID NO: 8)
STRAP-3	YVGGKRFILSPNLNW YLPAAYVLGLIIPCT VLVTKFVLIMPCVDN TLTIRLOGWERNKSH					128 (Portion of SEQ ID NO: 2)
STRAP-4	TYGWTAFEEESRYKF YIPPTFTXTLLVPCV RSSWAKALFXLPCIQ P-----					128 (Portion of SEQ ID NO: 8)

~~FIG. 14~~

FIG. 14A

26x

A

1 2 3 4 5 6 7 8



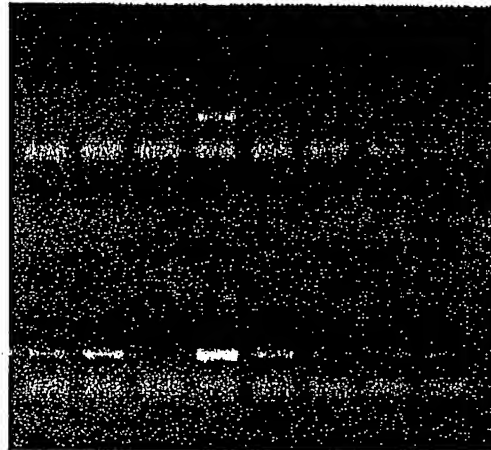
B

FIG. 14B

1 2 3 4 5 6 7 8

25x

30x

~~A~~

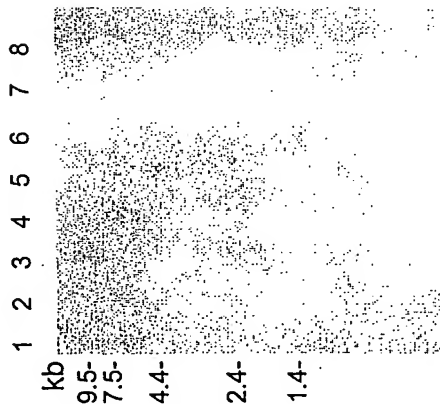
1. Brain
2. Prostate
3. LAPC-4 AD
4. LAPC-4 AI
5. LAPC-9 AD
6. HeLa
7. Murine cDNA
8. Neg. control

~~B~~

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

FIG. 15

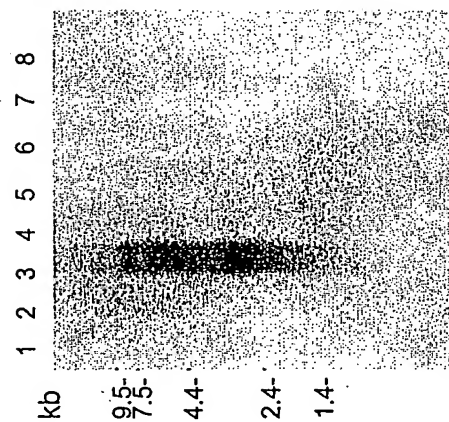
FIG. 15A



A-

1. Heart
2. Brain
3. Placenta
4. Lung
5. Liver
6. Skeletal Muscle
7. Kidney
8. Pancreas

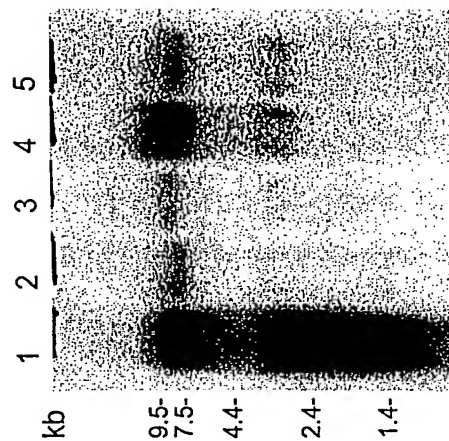
FIG. 15B



B-

1. Spleen
2. Thymus
3. Prostate
4. Testis
5. Ovary
6. Small Intestine
7. Colon
8. Leukocytes

FIG. 15C



C-

1. Prostate
2. LAPC-4 AD
3. LAPC-4 AI
4. LAPC-9 AD
5. LAPC-9 AI

FIG. 17

GDB Compreher

